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Gencore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 00:18:43 ; Search time 3:175 Seconds

(Without alignments)
1668 255 Million cell updates/sec

Title: US-09-762-105-14

Perfect score: 182

Sequence: 1 gagctcgctcccgccgtc.....tgacttgccaggctgc 182

Scoring Table: IDENTITY_NUC Gapext 1.0

Searched: 205640 seqs., 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.4

1: gb_gb.*

2: gb_hgt.*

3: gb_in.*

4: gb_cm.*

5: gb_cv.*

6: gb_pc.*

7: gb_ph.*

8: gb_pr.*

9: gb_xo.*

10: gb_sts.*

11: gb_sy.*

12: gb_vl.*

13: gb_vn.*

14: gp_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_cm.*

21: em_or.*

22: em_cv.*

23: em_pt.*

24: em_ph.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

28: em_vl.*

29: em_un.*

30: em_hgt_hum.*

31: em_hgt_other.*

32: em_hgt_hum.*

33: em_hgt_Plh.*

34: em_hgt_Pdi.*

35: em_hgt_Nam.*

36: em_hgt_Ytc.*

37: em_hgt_Ytc.*

38: em_hgt_Ytc.*

39: em_hgt_hum.*

40: em_hgt_other.*

41: em_hgt_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB	ID	Description
c 1	182	100.0	5270	12	AF176637	Plastid t
c 2	111.2	61.1	168	6	AF076661	Sequence
c 3	85.8	47.1	127	6	AX137514	Sequence
c 4	85.8	47.1	127	6	BS11179	Method for
c 5	85.8	47.1	127	6	BS11197	Process for
c 6	85.8	47.1	766	8	AF01453	Tobacco (N.
c 7	85.8	47.1	2113	8	CHTRNL	Tobacco chl
c 8	85.8	47.1	3274	8	CHPTNIV	X70338 N.Plumbago
c 9	85.8	47.1	7829	8	CPV1834	Solanum nigrum
c 10	85.8	47.1	155939	8	CHPTXX	200044 Nicotiana t.
c 11	85.8	47.1	155939	8	AB331052	Atropa be
c 12	85.8	47.1	156687	8	AB331052	AB331052 Atropa be
c 13	85.8	47.1	156687	8	AR445194	AR445194 Sequence
c 14	85.4	46.9	184	6	AR445194	AR445194 Sequence
c 15	85.4	46.9	300	6	AR471710	AR471710 Sequence
c 16	85.4	46.9	300	6	AR471710	AR471710 Sequence
c 17	85.4	46.9	2962	12	XN112809	U12809 Transform
c 18	85.4	46.9	3019	12	XN112810	U12810 Transform
c 19	85.4	46.9	3019	12	XN112811	U12811 Transform
c 20	85.4	46.9	3136	12	AF061065	AF061065 Plastid t
c 21	85.4	46.9	4126	12	XN112812	U12812 Transform
c 22	85.4	46.9	4126	12	XN112813	U12813 Transform
c 23	85.4	46.9	4174	12	XN112814	U12814 Transform
c 24	85.4	46.9	4174	12	XN112815	U12815 Transform
c 25	85.4	46.9	4304	12	AF009806	AF009806 Transform
c 26	85.4	46.9	4454	12	CR312331	AJ12392 Chloroplast
c 27	85.4	46.9	7626	12	CR312332	AJ12393 Chloroplast
c 28	85.4	46.9	7626	12	CR312333	AJ12394 Chloroplast
c 29	84.8	46.6	159	12	M3201	M3201 Synthetic C
c 30	84.8	46.6	310	12	MJ200	X62199 E.coli Plas
c 31	84.8	46.6	2731	12	PE311P	X5204 Cloning vec
c 32	84.8	46.6	2829	12	CPB276C	X5205 Cloning vec
c 33	84.8	46.6	2829	12	CPB276C	X5206 Cloning vec
c 34	84.8	46.6	2830	12	CPB276B	X5207 Cloning vec
c 35	84.8	46.6	2831	12	CPB276A	X5208 Cloning vec
c 36	84.8	46.6	2831	12	CPB276A	X5209 Cloning vec
c 37	84.8	46.6	2894	12	CW7740	U22265 Expression
c 38	84.8	46.6	3984	12	I15535	I15535 Sequence 1
c 39	84.8	46.6	3993	12	X63317	X63317 Cloning vec
c 40	84.8	46.6	3995	12	X63318	X63318 Cloning vec
c 41	84.8	46.6	5231	6	AM001273	AM001273 Sequence
c 42	84.8	46.6	5953	6	AX91649	AX91649 Sequence
c 43	84.8	46.6	3937	7	T7CG	V01146 Genome of b
c 44	84.8	46.6	45	187	AF004778	AF004778 Sequence
c 45	83.2	45.7	187	6	AF004778	

ALIGNMENTS

Result 1	LOCUS	DEFINITION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
AF176637/c	AF176637	Plastid transformation vector pMSK9	1	5270 bp DNA linear	SYN 24-APR-2000				

Pred. No. is the number of results predicted by chance to have a

Sequence of a putative promoter region for the rRNA genes of tobacco chloroplast DNA
Nucleic Acids Res. 9 (20), 5399-5406 (1981)
70250514
709469
70250514
TRNA sequence contributed on tape April 1983 by M. Sprinzl & D. Gauß; from the entry 203 in Nucleic Acids Res. 11, r55-r1 (1983). The sequence is based on 308 or 308 as possible sites for transcription initiation, based on an in vitro assay with *E. coli* RNA polymerase.

11. Itoh, T., Shiozaki, K., and Suguri, M. Sequence of a putative promoter region for the rRNA genes of tobacco chloroplasts. *MEDLINE* 8211820 (2), 213-218 (1982)

12. Itoh, T., Shiozaki, K., and Suguri, M. REFERENCE 2 (bases 1 to 766)

13. Itoh, T., Shiozaki, K., and Suguri, M. AUTHORS Sequence of a putative promoter region for the rRNA genes of tobacco chloroplast DNA. *MEDLINE* 8211820 (2), 213-218 (1982)

JOURNAL	Submitted (27-PER-1998), T. Tsubuki, Data Processing Center, Aichi Gakuen University, 12, Arakie, Tawarak, Nisshin, Aichi, 470-0345, JAPAN	Accepted (20-APR-1999), T. Tsubuki, Data Processing Center, Aichi Gakuen University, 12, Arakie, Tawarak, Nisshin, Aichi, 470-0345, JAPAN	DOI: 10.1007/s00162-002-0264-9, Date: 17. 02. 2002 this sequence version replaced 91:264799, COMMENT: 011807
The circular tobacco chloroplast DNA sequence is presented in a linearized form by cutting at the junction (TJA) between tRNA and tRNA.			
lsc	lsc is designated zero and numbered proceeding towards LSC. The DNA strand which codes for the large subunit of ribulose 1,5-bisphosphate carboxylase is designated as strand and the complementary strand as B strand. tRNA	lsc	lsc is designated zero and numbered proceeding towards LSC. The DNA strand which codes for the large subunit of ribulose 1,5-bisphosphate carboxylase is designated as strand and the complementary strand as B strand. tRNA
atps1	1.15936 (866686 bp) Inverted complementary sequence of the lsc strand is presented.	atps1	1.15936 (866686 bp) Inverted complementary sequence of the lsc strand is presented.
atps2	Large single copy region (LSC) 1.15936 (866686 bp) Small single copy repeat B (tRNA) : 1.102027 (25341 bp) Inverted repeat A (tRNA) repeat SSC: 1.102028 - 1.105938 (10571 bp) An alphabetical index of tobacco chloroplast genes and ORFs. GENE	atps2	Large single copy region (LSC) 1.15936 (866686 bp) Small single copy repeat B (tRNA) : 1.102027 (25341 bp) Inverted repeat A (tRNA) repeat SSC: 1.102028 - 1.105938 (10571 bp) An alphabetical index of tobacco chloroplast genes and ORFs. GENE
atps3	NUCLEOTIDE NUMBER (FROM 5' TO 3')	atps3	NUCLEOTIDE NUMBER (FROM 5' TO 3')
atps4	1.18862	atps4	1.18862
atps5	1.21448	atps5	1.21448
atps6	5.67777	atps6	5.67777
atps7	5.78584	atps7	5.78584
atps8	1.31522	atps8	1.31522
atph	1.41999	atph	1.41999
atpi	1.61000	atpi	1.61000
atpp	7.40700	atpp	7.40700
atpp	8.09595	atpp	8.09595
atpp	8.10585	atpp	8.10585
atpp	1.20323	atpp	1.20323
atpp	9.96611	atpp	9.96611
atpp	5.26667	atpp	5.26667
atpp	1.19255	atpp	1.19255
atpp	1.19955	atpp	1.19955
atpp	1.14292	atpp	1.14292
atpp	1.20769	atpp	1.20769
atpp	1.15116	atpp	1.15116
atpp	1.21619	atpp	1.21619
atpp	1.21615	atpp	1.21615
atpp	5.94455	atpp	5.94455
atpp	5.98941	atpp	5.98941
atpp	1.021024	atpp	1.021024
atpp	1.06442	atpp	1.06442
atpp	1.108024	atpp	1.108024
atpp	1.146670	atpp	1.146670
atpp	9.61119,	atpp	9.61119,
atpp	6.61176	atpp	6.61176
atpp	6.75888	atpp	6.75888
atpp	3.51666	atpp	3.51666
atpp	1.94219	atpp	1.94219
atpp	1.45219	atpp	1.45219
atpp	1.07346	atpp	1.07346
atpp	1.17253	atpp	1.17253
atpp	1.11779	atpp	1.11779
atpp	1.16335	atpp	1.16335
atpp	7.7452	atpp	7.7452
atpp	7.04343	atpp	7.04343
atpp	6.6570	atpp	6.6570
atpp	6.6293	atpp	6.6293
psaA	4.48486	psaA	4.48486
psaB	4.12088	psaB	4.12088
psaC	1.13899	psaC	1.13899
psaI	6.02083	psaI	6.02083
psaJ	6.51595	psaJ	6.51595
psbA	7.9553	psbA	7.9553
psbB	3.55115	psbB	3.55115
psbC	3.44770	psbC	3.44770
psbD	6.71229	psbD	6.71229
psbE	6.66777	psbE	6.66777
psbH	7.7101	psbH	7.7101
psbI	8.398	psbI	8.398

RESULT	11	CHNTXX/C	CHNTXX	5' TCGCTCCGCCCTCTCTTCATGAGATGATANGAGCTCTGGATGAGCTGGG 64	circular PLN 27-JUL-2001
LOCUS				NCt00000000.1	155930 bp DNA
DEFINITION				chloroplast genome DNA	
ACCESSION	Db	102562	102562	TTCCTCCGCCCTCTCTTCATGAGATGATANGAGCTCTGGATGAGCTGGG 102621	
VERSION	QY	65	GGCAAGGATGACTATTCCTGGAGA 93		
KEYWORDS	Db	102622	102622	GGCAAGGATGACTATTCCTGGAGA 102650	
Query Match	47.1%		Score 85.8; Pred. No. 1.66-16;	length 155939;	
Best Local Similarity	97.8%		0; Mismatches 2;	Indels 0; Gaps 0;	
Matches 87; Conservative					
QY	5	TCGCTCCGCCCTCTCTTCATGAGATGATANGAGCTCTGGATGAGCTGGG 64			
Db	102562	TTCCTCCGCCCTCTCTTCATGAGATGATANGAGCTCTGGATGAGCTGGG 102621			
QY	65	GGCAAGGATGACTATTCCTGGAGA 93			
Db	102622	GGCAAGGATGACTATTCCTGGAGA 102650			
RESULT	11	CHNTXX/C	CHNTXX	5' TCGCTCCGCCCTCTCTTCATGAGATGATANGAGCTCTGGATGAGCTGGG 64	circular PLN 27-JUL-2001
LOCUS				NCt00000000.1	155930 bp DNA
DEFINITION				chloroplast genome DNA	
ACCESSION	Db	102562	102562	TTCCTCCGCCCTCTCTTCATGAGATGATANGAGCTCTGGATGAGCTGGG 102621	
VERSION	QY	65	GGCAAGGATGACTATTCCTGGAGA 93		
KEYWORDS	Db	102622	102622	GGCAAGGATGACTATTCCTGGAGA 102650	
Query Match	47.1%		Score 85.8; Pred. No. 1.66-16;	length 155939;	
Best Local Similarity	97.8%		0; Mismatches 2;	Indels 0; Gaps 0;	
Matches 87; Conservative					
QY	5	TCGCTCCGCCCTCTCTTCATGAGATGATANGAGCTCTGGATGAGCTGGG 64			
Db	102562	TTCCTCCGCCCTCTCTTCATGAGATGATANGAGCTCTGGATGAGCTGGG 102621			
QY	65	GGCAAGGATGACTATTCCTGGAGA 93			
Db	102622	GGCAAGGATGACTATTCCTGGAGA 102650			

סימן

on or before Jan 17, 2002 this sequence version replaced 91:26:799, 91:16000. A high molecular weight tobacco chloroplast DNA sequence is presented in a linearized form by cutting at the junction (J1A) between IRA and SC. SC. LSC is designated zero and numbered proceeding towards LSC. The DNA strand which codes for the large subunit of ribulose -5'-bisphosphate carboxylase is designated A strand and the complementary strand as B strand. The sequence of the LSC strand is presented in the following order: 1 - 86616 (86666 bp) Inverted repeat, 2 - 86616 (86666 bp) Inverted repeat, 3 - 86617 (115721 bp) Small single copy region (SSR), 4 - 1120128 (115721 bp) Inverted repeat A (IRA) region (SSA), 5 - 130599 (25341 bp) An alphabetical index of tobacco chloroplast genes and ORFS gene NUMBER (FROM NUCLEOTIDE NUMBER).

pspbm	30661	76899
pspbct	76895	76895
pspbcl	57985	57985
pspbcl1	88143	88143
pspbcl2	88143	88143
pspbcl3	85596	85596
pspbcl4	11616	11616
pspbcl5	71109	71109
pspbcl6	86550	86550
pspbcl7	154093	154093
pspbcl8	115631	115631
pspbcl9	70131	70131
pspbcl10	82655	82655
pspbcl11	81186	81186
pspbcl12	24793	24793
pspbcl13	115631	115631
pspbcl14	70131	70131
pspbcl15	82655	82655
pspbcl16	81186	81186
pspbcl17	24793	24793

59793	cccd	112612	rsr1	14469	rsr2	12448	tpa	56777	tpb	55884	tpc	13552	tcpf	11949	tcpb	16500	tp1	74507	tp2	84975	tp3	12305	tp4	12333	tp5	99261	tp6	143365	tp7	119025	tp8	119955	tp9	119dhd	tp10	119dhe	tp11	114392	tp12	120709	tp13	125116	tp14	126159	tp15	52165	tp16	49941	tp17	102202	tp18	46442	tp19	110824	tp20	131802	tp21	96556	tp22	146070	tp23	96119	tp24	146507	tp25	661176	tp26	67586	tp27	67586	tp28	124236	tp29	140524	tp30	110939	tp31	137776	tp32	1104718	tp33	117138	tp34	130606	tp35	119389	tp36	141208	tp37	67083	tp38	69565	tp39	1595	tp40	749043	tp41	68570	tp42	13486	tp43	119389	tp44	66866	tp45	771101	tp46	83395	tp47	66485	tp48	7835	tp49	66726	tp50
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SOURCE	Atropa belladonna
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Atropa.
REFERENCE	Schmitz Linneweber, C.; Regel, R.; Gia Du, T.; Hupfer, H.; Hermann, R.G. and Maier, R.M.
AUTHORS	The nucleotide sequence of the plastid chromosome of <i>Atropa belladonna</i> (deadly nightshade) and its comparison with that of <i>Nicotiana tabacum</i> with emphasis on sequence elements relevant for microevolution
TITLE	

mpublished
(bases 1 to 156687)
Schmitz-Linnnebecker, C.
Schmitz-Linnnebecker, C.
Submited (24-MAY-2000) Submited (24-MAY-2000)
Submitted, Ludwig Maximilians Universitat Munchen, Menzinger Str.
Institut, Ludwig Maximilians Universitat Munchen, Menzinger Str.
7, Munchen, Bavaria 80338, Germany
Location/Qualifiers
Location/Qualifiers

Diagram illustrating the genomic organization of a region. The genes (green boxes), tRNA (green box), and CDS (green and blue boxes) are shown with their exons (vertical bars) and introns (horizontal lines). Gene 1 and Gene 2 are on the left, tRNA 1 is in the middle, and CDS 1 and CDS 2 are on the right. Exons are colored green, and introns are colored red.

Belladonna
Atropa belladonna
Belladonna
Atropa belladonna
Viridiplanta; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euanasterids I; Solanaeae; Solanaceae; Atropa.
1
Schmitz-Linneweber, C., Regel, R., Gia Du T., Hufner, H., Herrmann, R.G. and Mair, J.M.
Schmitz-Linneweber, C., Regel, R., Gia Du T., Hufner, H., Herrmann, R.G. and Mair, J.M.
The nucleotide sequence of the plastid chromosome of Atropa belladonna (deadly nightshade) and its comparison with that of Nicotiana tabacum with emphasis on sequence elements relevant for plastid genome recombination

SOURCE	REFERENCE	JOURNAL	FEATURES
ORGANISM	AUTHORS	AUTHORS	SOURCE
	TITLE	TITLE	
		JOURNAL	

2002

-APR-
ATPase
-unit;
-gene;
-protein;
-subunit;
-chromo-
-NADH;
-NAD⁺;
-NADP⁺;
-NADP;
-ndh;
-none;
-none;
-peto;
(kan)

PLN 05
Ab5p
RNA;
a subunit;
mit; P
I; ATP;
atpB;
CCCSA F;
cema;
elongation;
cyto;
arase;
ubunit;
subunit;
subunit;
subunit;
subunit;
C gene;
gene
gene

osomal
e better
subun
ounit
gene;
ane; c
omes;
F comp
a b6;
matu
88kD su
32kD s
ND1 s
D3 sub
D4L s
ne; ndi
petD

DN
id Ch
RNA;
-COA
e; AT
unit;
atpB
subun
c-tyr
unit I
bit V;
ome f;
dehyd
dehyd
dehyd
gene;
gene;

7 bp
Plastid
rsosomal
acetyl
A gene
on sub
IV:
-ytic
ent to
subu
subu
cochrc
NADH
NADH
NADH
NADH
ndha
ndha

15668
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10
3 ribo-
ne; a-
t_{RNA}; atp;
epsilic
ubunit
catal
achemo-
complex
complex
cyt
unit;
pounit;
abunit;
unit;
unit;
unit;
gene
4489; v-

00068331
QA 239
cccd ge
to tease
phase e
ase su
gene;
e-att
6/f cc
f con
1
6 sub
kd su
kd su
2 sub
4 sub
5 sub
ndhf
OBF

GI:20
al RNA
aNA; ac-
ent pro-
t; AT-
atpI &
r hemm-
Cyt b
ome b
x sub-
se ND
se 19
se 49
se ND
se ND
se ND
se ND
gene;
gene;

BEE316
tropo
J3165
J3165
ri
6S ri
riboso
RTP-de
eta s
ubuni
tpH g
equir
lipP g
cytI
6/f
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WORLD 1
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 00:17:53 ; Search time 307 Seconds
(without alignments)

1335.061 Million cell updates/sec

Title: US-09-762-105-14

Perfect score: 182

Sequence: 1 ggatcgctcccgccgtc.....tgacttggacaggatgc 182

Scoring Table: IDENTITY.NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_GenSeq/0101002/*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	182	100.0	182	21	A261373
2	182	100.0	186	21	AA261384
c	164.4	100.0	516	21	AA261386
4	164.4	90.3	182	21	AA261374
5	159.4	87.6	161	21	AA261375
6	111.2	61.1	168	22	AA255755
7	111.2	61.1	168	22	AA255752
8	111.2	61.1	168	22	AA2557902
9	93.6	51.4	191	21	AA261361

ALIGNMENTS

Result No.	Query Match	Score	Length	DB ID	Description
10	93.6	51.4	227	21	A261360
11	93.6	51.4	227	21	A261362
12	93.6	51.4	104.9	22	A261268
13	93.6	51.4	198.5	21	A261382
14	92.2	50.7	153	21	A261369
15	92.2	50.7	185	21	A261372
16	92.2	50.7	195	21	A261368
17	90	49.5	130	22	A261256
18	90	49.5	131	22	A261259
19	90	49.5	154	21	A261164
20	90	49.5	159	21	A261366
21	90	49.5	195	21	A261365
22	90	49.5	195	21	A261367
23	90	49.5	196	21	A261363
24	90	49.5	195	21	A261371
25	89.6	49.2	171	16	A2614853
26	89	48.9	183	21	A261371
27	89	48.9	201	21	A261370
28	86.4	47.5	129	20	A261430
29	86	47.3	140	20	A261424
30	86	47.3	164	20	A261421
31	85.8	47.1	127	22	A261431
32	85.8	47.1	201	18	A2616101
c	33	85.8	47.1	6077	22
34	85.4	46.9	161	20	A261423
35	85.4	46.9	165	20	A261409
36	85.4	46.9	168	20	A261107
37	85.4	46.9	184	22	A269143
38	85.4	46.9	258	20	A261129
c	39	85.4	46.9	1334	18
c	40	85.4	46.9	1334	20
c	41	85.4	46.9	1183	21
c	42	85.4	46.9	1008	20
c	43	85.4	46.9	1416	20
c	44	85.4	46.9	1417	18
c	45	85.4	46.9	2962	20

RESULTS

Result No.	Query Match	Score	Length	DB ID	Description
1	10:	100.0	182	21	A261373
2	10:	100.0	186	21	A261373
c	164.4	100.0	516	21	A261371
4	164.4	90.3	182	21	A261374
5	159.4	87.6	161	21	A261375
6	111.2	61.1	168	22	AA255755
7	111.2	61.1	168	22	AA255752
8	111.2	61.1	168	22	AA2557902
9	93.6	51.4	191	21	A261361

ALIGNMENTS

Result No.	Query Match	Score	Length	DB ID	Description
1	10:	100.0	182	21	A261373
2	10:	100.0	186	21	A261373
c	164.4	100.0	516	21	A261371
4	164.4	90.3	182	21	A261374
5	159.4	87.6	161	21	A261375
6	111.2	61.1	168	22	AA255755
7	111.2	61.1	168	22	AA255752
8	111.2	61.1	168	22	AA2557902
9	93.6	51.4	191	21	A261361

RESULTS

ALIGNMENTS

Result No.	Query Match	Score	Length	DB ID	Description
1	10:	100.0	182	21	A261373
2	10:	100.0	186	21	A261373
c	164.4	100.0	516	21	A261371
4	164.4	90.3	182	21	A261374
5	159.4	87.6	161	21	A261375
6	111.2	61.1	168	22	AA255755
7	111.2	61.1	168	22	AA255752
8	111.2	61.1	168	22	AA2557902
9	93.6	51.4	191	21	A261361

RESULTS

ALIGNMENTS

Result No.	Query Match	Score	Length	DB ID	Description
1	10:	100.0	182	21	A261373
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c	164.4	100.0	516	21	A261371
4	164.4	90.3	182	21	A261374
5	159.4	87.6	161	21	A261375
6	111.2	61.1	168	22	AA255755
7	111.2	61.1	168	22	AA255752
8	111.2	61.1	168	22	AA2557902
9	93.6	51.4	191	21	A261361

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ALIGNMENTS

Result No.	Query Match	Score	Length	DB ID	Description
1	10:	100.0	182	21	A261373
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8	111.2	61.1	168	22	AA2557902
9	93.6	51.4	191	21	A261361

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ALIGNMENTS

Result No.	Query Match	Score	Length	DB ID	Description
1	10:	100.0	182	21	A261373
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c	164.4	100.0	516	21	A261371
4	164.4	90.3	182	21	A261374
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6	111.2	61.1	168	22	AA255755
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9	93.6	51.4	191	21	A261361

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Result No.	Query Match	Score	Length	DB ID	Description
1	10:	100.0	182	21	A261373
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c	164.4	100.0	516	21	A261371
4	164.4	90.3	182	21	A261374
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7	111.2	61.1	168	22	AA255752
8	111.2	61.1	168	22	AA2557902
9	93.6	51.4	191	21	A261361

RESULTS

ALIGNMENTS

Result No.	Query Match	Score	Length	DB ID	Description
1	10:	100.0	182	21	A261373
2	10:	100.0	186	21	A261373
c	164.4	100.0	516	21	A261371
4	164.4	90.3	182	21	A261374
5	159.4	87.			

FT	key_feature	7.176	Location/qualifiers
FT		/*tag: a	
FT		/*note: "m7 phage gene 10 downstream box"	
FT	misc_feature	218..1001	
FT		/*tag: b	
FT		/*note: "m7 phage gene 10 downstream box"	
FT	misc_feature	105..175	
FT		/*tag: c	
FT		/*note: "green fluorescent protein region"	
FT	misc_feature	1766..1934	
FT		/*tag: d	
FT		/*note: "psba region"	
XX			
PN	WO200007431-A1.		
XX			
PD	17-PB-2000.		
XX			
PF	03-AUG-1999;	90900-US17806.	
XX			
PR	03-AUG-1998;	90110-US0095163.	
PR	03-AUG-1998;	90110-US0095167.	
PR	15-DEC-1998;	90110-US0112257.	
PR	29-APR-1999;	90110-US011611.	
PR	11-JUN-1999;	90110-US0138764.	
XX			
PA	(RUTTER) UNIV RUTGERS STATE NEW JERSEY.		
XX			
PT	Malliga P, Kuroda H, Khan MS;		
XX			
DR	2000-205525/18.		
XX			
PR	Now recombinant DNA constructs, for expressing high level heterologous protein in plasmids of higher plants, including a leader sequence and a downstream box element -		
PR	XX		
PS	disclosure: Fig 32: 164P; English.		
XX			
CC	The present sequence represents a DNA construct of the		
CC	heterologous proteins in the recombinant C. canephora plants.		
CC	constructs are used for production of heterologous protein which include		
CC	a leader sequence and a downstream box element -		
CC	to a high level of the heterologous protein. The chimera enhances translational efficiency of an mRNA molecule.		
CC	For example, the DNA constructs are used for heterologous protein expression in monocot and dicot plants having high levels of heterologous protein expression.		
CC	They can be used to drive expression of proteins of agronomic, industrial or pharmaceutical importance, including		
CC	of vaccines, healthcare products like human monoclonal antibodies, household enzymes, plants which can be transformed into a		
CC	household invention, including plants which can be transformed into a		
CC	wheat, barley, oat, rye or turf grass.		
XX			
SO	Sequence 1961 BP; 552 A; 430 C; 486 G; 493 T; 0 other;		
Query Match	100.0%	Score: 182;	DB: 21; Length:
Best Local Similarity	100.0%	Pred. No. 2	9E-50;
Matches	12;	0; Mismatches	0;
Qy	1. GAGGTCGCGCCCGCGCGCGTCATAGTAAAGTAAAGGACTGCTGG		
Db	1. GAGGTCGCGCCCGCGCGTCATAGTAAAGTAAAGGACTGCTGG		
Qy	61. AGGGCGAGGAGGCGCTATATTCGGAGGAGCACACCGCTCC		
Db	61. AGGGCGAGGAGGCGCTATATTCGGAGGAGCACACCGCTCC		
Qy	121. ATTTGTTAAATTCGAGGAGTAAATATGCGAGGAGTACGTC		
Db	121. ATTTGTTAAATTCGAGGAGTAAATATGCGAGGAGTACGTC		
Qy	181. GC 182		

Mon Dec 16 13:20:22 2002

DE	DE	Nucleotide sequence of chimeric promoter <i>PrrnAtpb+DBm</i> .
KW	KW	Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin; Prrn promoter; atpb; protein expression; vaccine; enzyme; ss.
KW	KW	Prrn promoter; atpb; protein expression; vaccine; enzyme; ss.
OS	OS	Synthetic.
XX	XX	Key Location/Qualifiers
FT	FT	7 . 89
FT	FT	/*tag= a
FT	FT	/*note= "rrn Plastid promoter"
FT	FT	114 . 116
FT	FT	/*tag= b
FT	FT	/*note= "Shine-Dalgarno sequence"
XX	XX	DN WO200007431-A1.
XX	XX	FD 17 -FEB-2000.
XX	XX	FF 03 -AUG-1999; 99WO-US17806 .
XX	XX	PR 03 -AUG-1998; 99US 0095163 .
XX	XX	PR 03 -AUG-1998; 99US 0095167 .
PR	PR	15 -OCT-1998; 99US 011257 .
PR	PR	29 -APR-1999; 99US 013161 .
PR	PR	11 -JUN-1999; 99US 0138764 .
XX	XX	PA (RUTF) UNIV RUTGERS STATE NEW JERSEY .
XX	XX	PI Maliga P, Kuroda H, Khan MS;
XX	XX	DR WPI; 2000-205525/18
XX	XX	XX New recombinant DNA constructs, for expressing high levels of heterologous protein in plastids of higher plants, includes promoter, a leader sequence and a downstream box element - claim 3: Fig 3a: 164pp: English.
XX	XX	XX The present sequence represents a chimeric plastid rRNA operon omega-type (Prrn) promoter with atpb translation control sequences and a mutated downstream box. The chimeric promoter is used as a 5' regulatory sequence to produce recombinant DNA constructs for expressing heterologous proteins in the plastids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter element, a leader sequence and a downstream box element originally linked to a coding region of the heterologous protein. The chimeric regulatory region enhances translational efficiency of an mRNA molecule encoded by the DNA construct. The DNA constructs are used for producing transformed monocot and dicot plants having high levels of heterologous protein expression. They can be used to live expression of proteins with agronomic, industrial or pharmaceutical importance, including production of vaccines, healthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.
XX	XX	Sequence 227 BP: 64 A: 40 C: 59 G: 64 T: 0 other: 51 . 48 : Score 93 . 6 : DB 21: Length 227; Best Local Similarity 75 . 0% : Prec. NO. 3e-19; Gaps 0;
Qy	Qy	Matches 117: Conservative 0; Mismatches 39; Indels 0; Gaps 1
Db	Db	1 GAGCCTCCTCCCTCCCTCGTCATCAATGAGAATGATAGGCTGCGGATGACGTCG 60
Qy	Qy	1 GAGCCTCCTCCCTCCCTCGTCATCAATGAGAATGATAGGCTGCGGATGACGTCG 60
Db	Db	61 AGGGAGGAGGAGGAGGATGCTATTCGCGGAGGAGGACCAACGCGTTCCTGAGAATA 120
Qy	Qy	61 AGGGAGGAGGAGGAGGATGCTATTCGCGGAGGAGGACCAACGCGTTCCTGAGAATA 120
121 ATTTGCTTAACTTGTAGGAGGAGGATGATATGG 156		

xx	Sequence 185 BP; 47 A; 35 C; 51 G; 52 T; 0 other;
SO	Score: 92.7; DB: 21; length: 185;
Query Match	Score: 92.7; DB: 21;
Similarity	90.7%; Pred: No. 8.1e-18;
Berkeley	98.8%; Conservative: 0;
Matches	Mismatches: 13; Indels: 0;
100;	Gaps: 0;
Qy	1 GACCTGCTGCCCGCTTCATAGAGATGATGAGCTGAGCTGAGCTCCG 60
1 GACCTGCTGCCCGCTTCATAGAGATGATGAGCTGAGCTGAGCTCCG 60	1 GACCTGCTGCCCGCTTCATAGAGATGATGAGCTGAGCTGAGCTCCG 113
Db	1 GACCTGCTGCCCGCTTCATAGAGATGATGAGCTGAGCTGAGCTCCG 113
Qy	61 AGCTGGCTGGATGCTTATTTCTGGGAAAGACCTTCACTTTATTT 113
61 AGCTGGCTGGATGCTTATTTCTGGGAAAGACCTTCACTTTATTT 113	61 AGCTGGCTGGATGCTTATTTCTGGGAAAGACCTTCACTTTATTT 113

Search completed: December 15, 2002, 00:32:45
Time taken: 111.99s

Result No.	Query Score	Match Length	DB ID	Description
1	89.6	49.2	171 1	US-08-217-360-16
2	86.4	47.5	129 2	US-08-189-226A-25
3	86.4	47.3	149 4	US-09-193-833-25
4	86	47.3	140 2	US-08-189-226A-19
5	86	47.3	140 4	US-09-193-833-19
6	86	47.3	164 2	US-08-189-226A-26
7	86	47.3	164 4	US-09-193-833-26
8	85.4	46.9	161 2	US-08-189-226A-18
9	85.4	46.9	161 4	US-09-193-833-18
10	85.4	46.9	165 2	US-08-189-226A-4
11	85.4	46.9	165 4	US-09-193-833-4
12	85.4	46.9	168 2	US-08-189-226A-2
13	85.4	46.9	168 4	US-09-193-833-2
14	85.4	46.9	184 4	US-09-193-819-3
15	85.4	46.9	184 2	US-09-193-819-3
16	85.4	46.9	259 2	US-08-189-226A-24
17	85.4	46.9	300 4	US-08-202-316-4
18	85.4	46.9	134 2	US-08-189-226A-10
C 20	85.4	46.9	113 4	US-09-193-833-10
C 21	85.4	46.9	114 3	US-09-193-814-6
C 22	85.4	46.9	120 2	US-08-189-226A-28
C 23	85.4	46.9	120 4	US-09-189-226A-28
C 24	85.4	46.9	116 2	US-08-189-226A-27
C 25	85.4	46.9	116 4	US-09-193-851-27
C 26	85.4	46.9	117 4	US-09-142-114B-7
C 27	85.4	46.9	2962 2	US-08-189-256A-3

Copyright (C) 1993 - 2002 Compugen Ltd.	GenCore version 5.1.3
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Percent score: 182	
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Total number of hits satisfying chosen Parameters: 882724	
Maximum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	
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3: /cn2.6/ptodata/2/lna/6A_COMB_secl:*	
4: /cn2.6/ptodata/2/lna/6B_COMB_secl:*	
5: /cn2.6/ptodata/2/lna/FC1US_COMB_secl:*	
6: /cn2.6/ptodata/2/lna/backfile1_secl:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	89.6	49.2	171 1	US-08-217-360-16
2	86.4	47.5	129 2	US-08-189-226A-25
3	86.4	47.3	149 4	US-09-193-833-25
4	86	47.3	140 2	US-08-189-226A-19
5	86	47.3	140 4	US-09-193-833-19
6	86	47.3	164 2	US-08-189-226A-26
7	86	47.3	164 4	US-09-193-833-26
8	85.4	46.9	161 2	US-08-189-226A-18
9	85.4	46.9	161 4	US-09-193-833-18
10	85.4	46.9	165 2	US-08-189-226A-4
11	85.4	46.9	165 4	US-09-193-833-4
12	85.4	46.9	168 2	US-08-189-226A-2
13	85.4	46.9	168 4	US-09-193-833-2
14	85.4	46.9	184 4	US-09-193-819-3
15	85.4	46.9	184 2	US-09-193-819-3
16	85.4	46.9	259 2	US-08-189-226A-24
17	85.4	46.9	300 4	US-09-193-833-24
18	85.4	46.9	300 4	US-09-202-316-4
C 20	85.4	46.9	134 2	US-08-189-226A-10
C 21	85.4	46.9	113 4	US-09-193-833-10
C 22	85.4	46.9	114 3	US-09-193-814-6
C 23	85.4	46.9	120 2	US-08-189-226A-28
C 24	85.4	46.9	120 4	US-09-189-226A-28
C 25	85.4	46.9	116 2	US-09-193-851-27
C 26	85.4	46.9	117 4	US-09-142-114B-7
C 27	85.4	46.9	2962 2	US-08-189-256A-3

ALIGNMENTS

RESULT 1 US-08-217-360-16	Sequence 16, Application US/08217360
	Patent No. 550191
	GENERAL INFORMATION:
	APPLICANT: MALICA, Paul
	TITLE OF INVENTION: METHODS FOR PRODUCING CYTODIPLASMIC STABILITY IN PLANTS AND USE THEREOF IN PRODUCTION OF H
	TITLE OF INVENTION: MALE STERILITY IN PLANTS
	TITLE OF INVENTION: SEED
	NUMBER OF SEQUENCES: 17
	CORRESPONDENCE ADDRESS:
	DANIEL BORFMAN, Herrell and Skillman, P.C.
	STREET: 1601 Market Street, Suite 7200
	CITY: Philadelphia
	STATE: PA
	ZIP: 19103-2307
	COMPUTER READABLE FORM:
	SOFTWARE: Patentin Release #1.0, Version #1.25
	COMPUTER: IBM PC compatible
	OPERATING SYSTEM: PC-DOS/MS-DOS
	SOFTWARE: Floppy disk
	CURRENT APPLICATION DATA:
	APPLICATION NUMBER: US/08/217,360
	FILING DATE: 24-MAR-1994
	CLASSIFICATION: 800
	ATTORNEY/AGENT INFORMATION:
	NAME: REED, Janet E.
	REGISTRATION NUMBER: 36,252
	REFERENCE/DOCKET NUMBER: Rutgers University
	TELECOMMUNICATION INFORMATION:
	TELEPHONE: (215)563-4044
	FAX: (215)533-4044
	TELETYPE:
	INFORMATION FOR SEQ ID NO: 16:
	SEQUENCE CHARACTERISTICS:
	LENGTH: 171 base pairs
	TYPE: nucleic acid
	STRANDEDNESS: single
	TOPOLOGY: linear
	MOLECULE TYPE: DNA (genomic)
	HYPOTHETICAL: NO
	ANTI-SENSE: NO
	US-08-217-360-16

Query Match Score 89.6; Length 171;

Best Local Similarity 78.3%; Fred. No. 1.3e-21;

Mismatches 0; Indels 22;

Matches 130; Conservative 0;

Gaps 14;

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Sequence 3, Appli

Sequence 10, Appli

Sequence 11, Appli

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Sequence 14

Mon Dec 16 13:20:23 2002

STREET: 1601 Market Street Suite 720
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-2307
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/193 853
 FILING DATE: 08/18/98
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/189,256A
 FILING DATE: 31-JAN-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/111,398
 FILING DATE: 25-AUG-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,763
 FILING DATE: 01-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 561-4044
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 US-08-189-256A-18

Query Match 99% Score 85.4; DB 2; Length 161;
 Best Local Similarity 98%; Pred. No. 3.Se-20;
 Matches 86; Conservative 0; Indels 0; Gaps 0;
 Qy 7 GTCGCCCGCGCTGCTCAATGAGATAGCTGGGATGAGCTGGGG 66
 Db 23 GCTCCCGCCGGTGTCTGATGAGGGCTCGTGGATGAGGGG 82

Query Match 98% Score 85.4; DB 2; Length 161;
 Best Local Similarity 98%; Pred. No. 3.Se-20;
 Matches 86; Conservative 0; Indels 0; Gaps 0;
 Qy 7 GTCGCCCGCGCTGCTCAATGAGATAGCTGGGATGAGCTGGGG 66
 Db 23 GCTCCCGCCGGTGTCTGATGAGGGCTCGTGGATGAGGGG 82

Query Match 93% Score 85.4; DB 2; Length 161;
 Best Local Similarity 93%; Pred. No. 3.Se-20;
 Matches 86; Conservative 0; Indels 0; Gaps 0;
 Qy 67 CAGGGATGCGTATATTCGGGAGGA 93
 Db 83 CAGGGATGCGTATATTCGGGAGGA 109

RESULT 9
 US-09-193-853-18 Application US/09193853
 GENERAL INFORMATION:
 Patent No. 638168
 APPLICANT: Maliga, Pal
 APPLICANT: Svab, Zora
 APPLICANT: Staub, Jeffrey
 APPLICANT: Zoubek, Oleg V.
 APPLICANT: Allison, Lorin A.
 APPLICANT: Carrer, Helaine
 APPLICANT: Kaneko, Ivan
 TITLE OF INVENTION: DNA Constructs and Methods for Stably Transforming Plastids of Multicellular Plants and Expressing Recombinant Proteins Therein
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Darn, Dorrell and Skillman
 STREET: 1601 Market Street Suite 720
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-2307

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/189,256A
 FILING DATE: 31-JAN-1994
 CLASSIFICATION: 5

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/111,398
 FILING DATE: 25-NOV-1993
 PRIOR APPLICATION NUMBER: US/07/518,763
 FILING DATE: 01-MAY-1994
 ATTENDEE: AGENT INFORMATION:

NAME: Reed, Janet E. 36,252
 REGISTRATION NUMBER: 36,252

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 63-4100
 TELEFAX: (215) 63-4044

INFORMATION FOR SEQ. ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 165
 BASE PAIRS: 165
 NUMBER OF BASE PAIRS: 165

PATENTABILITY:

DEPENDENCY: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-189-256A-4

Query Match Score: 95.4%; DB: 2; Length: 165;
 Best Local Similarity: 96.9%; Score: 95.4%; DB: 2; Length: 165;
 Matches: 66; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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Qy 7 GCTGCCCCCGTGTCTGTCATGAGTAAAGATGATAGCTCGATGAGCTGAGGG 66
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Query Match Score: 93%; DB: 2; Length: 165;
 Best Local Similarity: 96.9%; Score: 93%; DB: 2; Length: 165;
 Matches: 66; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Matches 1: 1 GAGGGAGCTATTCGAGGGA 93

Qy 67 CAGGGAGCTATTCGAGGGA 93
 Db 61 CAGGGAGCTATTCGAGGGA 87

RESULT 11

US 09-191-953-4
 Sequence 4, Application US/09193853

GENERAL INFORMATION:

Patent No. 6381168
 Inventor: Maliga, Pal

APPLICANT: Maliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zelený, Oleg A. V.

APPLICANT: Zelený, O.

APPLICANT: Carrasco, Helaine

APPLICANT: Kaneko, Ivan

APPLICANT: DNA Constructs and Methods for Stably Transforming Plasmids of Multicellular Plants and Expressing Recombinant Proteins Therein

TYPE OF INVENTION: Transferring Plasmids of Multicellular Plants and Expressing Recombinant Proteins Therein

TITLE OF INVENTION: Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Danna, Horrell and Skillman
 STREET: 1600 Market Street Suite 720
 CITY: Philadelphia
 STATE: PA
 COUNTY: USA
 ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC/MS-DOS

SOFTWARE: Patents/Release #1.0, Version 1.1.30

CURRENT APPLICATION NUMBER: US/09/193,1853

APPLICATION NUMBER: US/09/193,1853

CLASSIFICATION:

PRIOR APPLICATION DATA:

TITLE OF INVENTION: DNA Constructs and Methods for Stably Transforming Plastids of Multicellular Plants and Expressing Recombinant Proteins Therein
TITLE OF INVENTION: 47
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunn, Dorman, Herrill and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102-2007
COMMERICAL NAME/ TRADE NAME:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 35
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 504-0000
TELEFAX: (215) 504-0044
SERIAL NUMBER FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-24

Query Match: 45.9%; Score 85.4; DB 2; Length 258;
Best Local Similarity: 93.9%; Pred. No. 4, 3e-20; Indels: 0; Gaps: 0;
Matches: 86; Conservative: 0; Mismatches: 1;
Ov 7 GCTCCCGCGCGTCGTCAATGAGAATGGATAGAGCTGATGATGCTGCGCG 66
Db 17 GCTCCCGCGCGTCGTCAATGAGAATGGATAGAGCTGATGCTGCGCG 76
Ov 67 CAGGATGCGTAATTCGGAGCA 93
Db 77 CAGGATGCGTAATTCGGAGCA 103

search completed: December 15, 2002, 02:07:54
Job time: 68 sec/s

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 01:28:19 ; Search time 88 Seconds

(without alignments)
817.885 Million cell updates/sec

Title: US-09-762-105-14

Sequence: 1: GAGCTCTCCCGCGTC.....Tgactgtggacaggctac 182

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640

Perfect score: 182

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-NA*

1: /cgn2_6/ptodata/2/pubpna/0507_PUBCOMB.seq;*
2: /cgn2_6/ptodata/2/pubpna/0511_NEW_PUB.seq;*
3: /cgn2_6/ptodata/2/pubpna/0506_NEW_PUB.seq;*
4: /cgn2_6/ptodata/2/pubpna/0507_NEW_PUB.seq;*
5: /cgn2_6/ptodata/2/pubpna/0507_NEW_PUB.seq;*
6: /cgn2_6/ptodata/2/pubpna/0508_NEW_PUB.seq;*
7: /cgn2_6/ptodata/2/pubpna/0510_NEW_PUB.seq;*
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10: /cgn2_6/ptodata/2/pubpna/0505_NEW_PUB.seq;*
11: /cgn2_6/ptodata/2/pubpna/0510_NEW_PUB.seq;*
12: /cgn2_6/ptodata/2/pubpna/0510_NEW_PUB.seq;*
13: /cgn2_6/ptodata/2/pubpna/0560_NEW_PUB.seq;*
14: /cgn2_6/ptodata/2/pubpna/0560_NEW_PUB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	77.8	202	10	US-09-843-1244-1	Sequence 1, Appli
2	77.8	244	10	US-09-843-1244-2	Sequence 2, Appli
3	69.2	38.0	39	US-09-843-416-12	Sequence 3, Appli
4	67.6	37.1	5018	9	Sequence 4, Appli
5	66.8	36.7	1057	9	Sequence 5, Appli
6	66.8	36.7	1098	9	Sequence 6, Appli
7	66.8	36.7	1217	9	Sequence 7, Appli
8	66.8	36.7	1217	9	Sequence 8, Appli
9	66.8	36.7	1238	9	Sequence 9, Appli
10	66.8	36.7	1238	9	Sequence 10, Appli
11	66.8	36.7	1238	9	Sequence 11, Appli
12	66.8	36.7	1241	9	Sequence 12, Appli
13	66.8	36.7	1241	9	Sequence 13, Appli
14	66.8	36.7	1241	9	Sequence 14, Appli
15	66.8	36.7	1282	9	Sequence 15, Appli
16	66.8	36.7	1285	9	Sequence 16, Appli
17	66.8	36.7	1301	9	Sequence 17, Appli
18	66.8	36.7	4102	9	Sequence 18, Appli
19	66.4	36.5	4682	9	Sequence 19, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	77.8	202	10	US-09-843-1244-1	Sequence 1, Appli
2	77.8	244	10	US-09-843-1244-2	Sequence 2, Appli
3	69.2	38.0	39	US-09-843-416-12	Sequence 3, Appli
4	67.6	37.1	5018	9	Sequence 4, Appli
5	66.8	36.7	1057	9	Sequence 5, Appli
6	66.8	36.7	1098	9	Sequence 6, Appli
7	66.8	36.7	1217	9	Sequence 7, Appli
8	66.8	36.7	1217	9	Sequence 8, Appli
9	66.8	36.7	1238	9	Sequence 9, Appli
10	66.8	36.7	1238	9	Sequence 10, Appli
11	66.8	36.7	1238	9	Sequence 11, Appli
12	66.8	36.7	1241	9	Sequence 12, Appli
13	66.8	36.7	1241	9	Sequence 13, Appli
14	66.8	36.7	1282	9	Sequence 14, Appli
15	66.8	36.5	4682	9	Sequence 15, Appli
16	66.8	36.7	1285	9	Sequence 16, Appli
17	66.8	36.7	1301	9	Sequence 17, Appli
18	66.8	36.7	4102	9	Sequence 18, Appli
19	66.4	36.5	4682	9	Sequence 19, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	SEQUENCE	TYPE	ORGANISM	FEATURE	OTHER INFORMATION
1	US-09-843-324A-1	Patent	US-09-843-324A	Patent	US-09-843-324A
	Sequence 1, Appli				Sequence 1, Application US-09843324A
	Sequence 10, Appli				Sequence 10, Application US-09843324A
	Sequence 9, Appli				Sequence 9, Application US-09843324A
	Sequence 6, Appli				Sequence 6, Application US-09843324A
	Sequence 5, Appli				Sequence 5, Application US-09843324A
	Sequence 4, Appli				Sequence 4, Application US-09843324A
	Sequence 3, Appli				Sequence 3, Application US-09843324A
	Sequence 2, Appli				Sequence 2, Application US-09843324A
	Sequence 1, Appli				Sequence 1, Application US-09843324A
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	Sequence 99, Appli				Sequence 99, Application US-09843324A
	Sequence 100, Appli				Sequence 100, Application US-09843324A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	SEQUENCE	TYPE	ORGANISM	FEATURE	OTHER INFORMATION
1	US-09-843-324A-1	Patent	US-09-843-324A	Patent	US-09-843-324A
	Sequence 1, Appli				Sequence 1, Application US-09843324A
	Sequence 2, Appli				Sequence 2, Application US-09843324A
	Sequence 3, Appli				Sequence 3, Application US-09843324A
	Sequence 4, Appli				Sequence 4, Application US-09843324A
	Sequence 5, Appli				Sequence 5, Application US-09843324A
	Sequence 6, Appli				Sequence 6, Application US-09843324A
	Sequence 7, Appli				Sequence 7, Application US-09843324A
	Sequence 8, Appli				Sequence 8, Application US-09843324A
	Sequence 9, Appli				Sequence 9, Application US-09843324A
	Sequence 10, Appli				Sequence 10, Application US-09843324A
	Sequence 11, Appli				Sequence 11, Application US-09843324A
	Sequence 12, Appli				Sequence 12, Application US-09843324A
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	Sequence 19, Appli				Sequence 19, Application US-09843324A
	Sequence 20, Appli				Sequence 20, Application US-09843324A
	Sequence 21, Appli				Sequence 21, Application US-09843324A
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	Sequence 26, Appli				Sequence 26, Application US-09843324A
	Sequence 27, Appli				Sequence 27, Application US-09843324A
	Sequence 28, Appli				Sequence 28, Application US-09843324A
	Sequence 29, Appli				Sequence 29, Application US-09843324A
	Sequence 30, Appli</td				

RESULT 6
 US-09-987-107-49
 Db 36 AGGGAGCACACAGGTTCCCTAGAAATTCTTAACTTAAAGGGATAT 95
 Qy 149 ACATATGGCA 158
 Db 96 ACATATGGCA 105

RESULT 6
 US-09-987-107-49
 ; Sequence 49, Application US/09987107
 ; Patent No. US20020156007A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAVERSEN, Jonas
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
 ; FILE REFERENCE: GRAVERSENIA
 ; CURRENT APPLICATION NUMBER: US/09/987,107
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/264,022
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: DK PA2001 00057
 ; PRIOR FILING DATE: 2001-01-15
 ; PRIOR APPLICATION NUMBER: DK PA2000 01682
 ; PRIOR FILING DATE: 2000-11-10
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 49
 ; LENGTH: 1088
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PTTH6 Trip-A-Apo A-1-de 43 - AmpR plasmid
 ; NAME/KEY: CDS
 ; LOCATION: (100) . (918)
 ; OTHER INFORMATION:
 US-09-987-107-49

Query Match % 36.7% ; Score 66.8 ; DB 9 ; Length 1088 ;
 Best Local Similarity 97.1% ; Pred. No. 2.5e-12 ; Indels 0 ; Gaps 0 ;
 Matches 68 ; Conservative 0 ; Mismatches 12 ; InDel 0 ; Gaps 0 ;
 Qy 89 AGGGAGCACACAGGTTCCCTAGAAATTCTTAACTTAAAGGGATAT 148
 Db 36 AGGGAGCACACAGGTTCCCTAGAAATTCTTAACTTAAAGGGATAT 95

RESULT 7
 US-09-987-107-47
 ; Sequence 47, Application US/09987107
 ; Patent No. US20020156007A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAVERSEN, Jonas
 ; APPLICANT: MOISTRUP, Soren
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
 ; FILE REFERENCE: GRAVERSENIA
 ; CURRENT APPLICATION NUMBER: US/09/987,107
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/264,022
 ; PRIOR FILING DATE: 2001-01-15
 ; PRIOR APPLICATION NUMBER: DK PA2000 01682
 ; PRIOR FILING DATE: 2000-11-10
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 47
 ; LENGTH: 1217
 ; TYPE: DNA

RESULT 8
 US-09-987-107-53
 ; Sequence 53, Application US/09987107
 ; Patent No. US20020156007A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAVERSEN, Jonas
 ; APPLICANT: MOISTRUP, Soren
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
 ; FILE REFERENCE: GRAVERSENIA
 ; CURRENT APPLICATION NUMBER: US/09/987,107
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/264,022
 ; PRIOR FILING DATE: 2001-01-15
 ; PRIOR APPLICATION NUMBER: DK PA2001 00057
 ; PRIOR FILING DATE: 2000-11-10
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 53
 ; LENGTH: 1217
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (100) . (1047)
 ; OTHER INFORMATION:
 US-09-987-107-53

Query Match % 36.7% ; Score 66.8 ; DB 9 ; Length 1217 ;
 Best Local Similarity 97.1% ; Pred. No. 2.6e-12 ; Indels 0 ; Gaps 0 ;
 Matches 68 ; Conservative 0 ; Mismatches 12 ; InDel 0 ; Gaps 0 ;
 Qy 89 AGGGAGCACACAGGTTCCCTAGAAATTCTTAACTTAAAGGGATAT 148
 Db 36 AGGGAGCACACAGGTTCCCTAGAAATTCTTAACTTAAAGGGATAT 95

RESULT 9
 US-09-987-107-55
 ; Sequence 55, Application US/09987107
 ; Patent No. US20020156007A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAVERSEN, Jonas
 ; APPLICANT: MOISTRUP, Soren
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
 ; FILE REFERENCE: GRAVERSENIA

Mon Dec 16 13:20:24 2002

us-09-762-105-14.rnpb

Page 6

Search completed: December 15, 2002, 03:13:31
Job time : 92 secs

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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 00:24:28 ; Search time 2428 Seconds

(without alignments)
1213.994 Million cell updates/sec

Title: US-09-762-105-14

Sequence: 1 gggctcgcccccgcgcgc.....tgactgtggacaggctacg 182

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16134066 seqs, 8097743.376 residues

Total number of hits satisfying chosen parameters:

32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST,*

1: em.estba,*

2: em.estbhun,*

3: em.estbm,*

4: em.estbm,*

5: em.estbm,*

6: em.estcp1,*

7: em.estro,*

8: em.est,*

10: gb.est1,*

12: gb.est3,*

13: gb.est4,*

14: gb.est5,*

15: em.estbm,*

16: em.estbm,*

17: em.gss_hum,*

18: em.gss_inv,*

20: em.gss_pln,*

21: em.gss_vrt,*

22: em.gss_fun,*

23: em.gss_mam,*

24: em.gss_mus,*

25: em.gss_other,*

26: em.gss_pro,*

27: em.gss_lod,*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	Match DB ID	Description
1	72.6	39.9	787	BH558942
2	72.4	39.8	775	BH558942
3	72.2	39.7	735	BH558942
4	72.2	39.7	838	BH472349
5	71.8	39.5	17	BH668002
6	71.8	39.5	836	BH709230

RESULT 1

BH558942 LOCUS BH558942 787 bp DNA linear clone BOHL272, DNA DEFINITION sequence.

ACCESSION BH558942.1 VERSION GI:17810722

KEYWORDS GSS, Brassica oleracea

ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Marcheophytina;

Spermatophytina; Magnoliophytina; Eudicotyledonae; Rosidae; Malpighiales; Malpighiidae; Brassicaceae; Brassicae.

REFERENCE 1 (bases 1 to 787) Town, C.D., Van Allen, S., Utterback, T., and Fraser, C.M., Whole genome shotgun sequencing of Brassica oleracea

JOURNAL Other GSS: BOHL272PF
COMMENT Contact: Chris town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-5523

Fax: 301-838-0208

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Unpublished ends

Location/Qualifiers 1 .787
source

ALIGNMENTS

BH653765 BONM137F

BH18480 BOCX95TR

BH471481 BOH7117P

BH72150 BONM124P

AQ362940 LERK124P

BH531952 BOCG338TR

BH677595 BOCM139TR

BH675997 BOH5137F

BH74703 BOCG197F

BH474703 BOCM120TR

BH646726 BOCM120TR

BH78091 BONM220TR

BH70526 BOMA313TR

BH57205 BOMF126TR

BH89289 BOML157TR

BH93122 BOHA338TR

BH664090 BOCM139TR

BH662193 BOMM129TR

BH552132 BOCG177F

BH533681 BOCM139TR

BH541572 BOCG177F

BH71072 C344110_b

BH78091 BOMM120TR

BH18884 BOMM121TR

BH669310 BOMM221TR

BH70036 BOCG143TR

BH69351 BOCM139TR

BH67597 BOH5137F

BH552132 BOCG177F

BH541147 BOCG177F

BH740722 C344110_b

BH78091 BOMM120TR

BH71072 C344110_b

BH68984 BOMM121TR

BH669310 BOMM221TR

BH70036 BOCG143TR

BH69351 BOCM139TR

BH67597 BOH5137F

BH714722 C344110_b

<p

FEATURES	source	Match 5 BH668002 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Matches 79; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Qy 3 GTCGCTCCGGCGCCTCGTCATAAGGATAGAGTAAAGCTGGATGAGCTGGTGGAG 62 Db 1 GCTGTCCTCGTCGTGATCCAAATGAGTAAAGCTGGATGAGCTGGTGGAG 60
			DNA is from a doubled haploid provided by Tom Osborn. Seq. primer: TF Class: sheared ends. Location/Qualifiers 1. 338 /organism="Brassica oleracea" /strain="R01000H3" /clone_id="Taxon_3712" /db_xref="B0145";
		RESULT 6 BH709230 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	836 bp DNA linear GSS 20-FEB-2002 BONNO33TR BO_2_3_KB Brassica oleracea genomic clone BONNO33, DNA sequence. BH709230 1 GI:18796385
			Bukarwala; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; euroids II; Brassicales; Brassicaceae; Brassica . REFERENCE 1 bases 1 to 836 AUTHORS Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. TITLE Whole genome shotgun sequencing of Brassica oleracea JOURNAL Unpublished (2001) COMMENT Other_GSS: BONNO33TF Contact: Chris Town TIGR Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-833-3523 Fax: 301-833-0208 Email: ctown@tigr.org
		FEATURES	Class: sheared ends. Location/Qualifiers 1. .836 /organism="Brassica oleracea" /strain="R01000H3"; /db_xref="Taxon_3712" /clone_id="BONNO33"; /clone_lib="BONNO33"; /note="Vector inserted into pBHSI; Site 1: BstXI; 2-3 kb sheared DNA inserted into pBHSI using BstXI linkers"
BASE COUNT	ORIGIN	BASE COUNT ORIGIN	BASE COUNT ORIGIN
		Query Match 39.7%; Score 72.2; DB 17; Length 838; Best Local Similarity 86.0%; Pred. No. 2.9e-12; Gaps 0; Matches 80; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	Query Match 39.5%; Score 71.8; DB 17; Length 836; Best Local Similarity 68.0%; Pred. No. 3.9e-12; Gaps 0; Matches 100; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
		Qy 4 CTCGCTCCGGCGCCTCGTCATAAGGATAGAGCTGGATGAGCTGGAG 63 Db 720 CTGTCCTCGTCGTGAGTCAGTAAAGGATAGAGCTGGATGAGCTGGAG 779	Qy 4 CTCGCTCCGGCGCCTCGTCATAAGGATAGAGCTGGATGAGCTGGAG 63 Db 664 CTGTCCTCGTCGTGAGTCAGTAAAGGATAGAGCTGGATGAGCTGGAG 779
		Qy 64 GGCAGGAGGTGTATTCGCGAGGAGC 96 Db 780 GGTCAGGTGACTTATTCGCGAGGAGC 812	Qy 64 GGCAGGAGGTGTATTCGCGAGGAGC 96 Db 724 GGTCAGGTGACTTATTCGCGAGGAGC 812
RESULT 5 BH668002 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE 1 (bases 1 to 770) AUTHORS Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. TITLE Whole genome shotgun sequencing of Brassica oleracea JOURNAL Unpublished (2001) COMMENT Contact: Chris Town TIGR Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-833-3523 Fax: 301-833-0208 Email: ctown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq. primer: TF Class: sheared ends. Location/Qualifiers 1. 770 /organism="Brassica oleracea" /strain="R01000H3"; /db_xref="Taxon_3712"; /clone_id="BONNO33"; /clone_lib="B0_2_3_KB"; /note="Vector: pBHSI Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pBHSI using BstXI linkers"	BASE COUNT ORIGIN	BASE COUNT ORIGIN
BASE COUNT	ORIGIN	Query Match 39.5%; Score 71.8; DB 17; Length 770; Best Local Similarity 86.8%; Pred. No. 3.9e-12;	Query Match 39.5%; Score 71.8; DB 17; Length 836; Best Local Similarity 68.0%; Pred. No. 3.9e-12; Gaps 0; Matches 100; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
		Qy 124 TTGTAACTTATGAGGAGTAC 150 Db 784 AACATGACTTGAATGAGAAATC 810	Qy 124 TTGTAACTTATGAGGAGTAC 150 Db 784 AACATGACTTGAATGAGAAATC 810
FEATURES	source	RESULT 7 BH653765 LOCUS DEFINITION	841 bp DNA linear GSS 19-FEB-2002 BONNX13TF BO_2_3_KB Brassica oleracea genomic clone BONNX13, DNA sequence. BH653765

Email: edtownsend@jif.org
 DNA is from aoubled haploid provided by Tom Osborn.

Seq primer: TF
 Class: sheared ends
 FEATURES source
 Location/Qualifiers
 1. .305
 /organism="Brassica oleracea"
 /strain="TOL0000DH3",
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 /clone_id="B0_2_3_KB",
 /vector="phos1",
 /site="BstXI; 2-3 kb sheared genomic DNA inserted into phos1 using BstXI linkers"
 BASE COUNT
 68 a 57 g 75 t
 ORIGIN

Query Match 38.9%; Score 70.8; DB 17; Length 305;
 Best Local Similarity 86.7%; Pred. No. 6e-12; Gaps 0;
 Matches 78; Conservative 0; Mismatches 12; Indels 0;
 QW 4 CTCGCTCCCGCCGCTCGCTCACTGAGAAATGGATAGAGCTCGTGGATTCAGTGAGG 63
 Db 102 CTCGCTCCCGCCGCTCGCTCACTGAGAAATGGATAGAGCTCGTGGATTCAGTGAGG 43
 QY 64 GGCAGGGATGGCTATAATTCTGGGAGGA 93
 Db 42 GGTAGGGTAGCTATTCCTGGAGCGA 13

Search completed: December 15, 2002, 02:06:36
 Job time : 2432 secs

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